## Figure 1A

1	GAGACAAAATTTCGAGGGTGGGATCCACTGAGGAGTACATAGACTGCTGGATTCTGGTGG	60
61	AGCCAGACACTGGTCCCAACGGGTGGTATCTGGCTCCTGTGGAGGGGGGTACGTGAGGGG	120
.21	GGGGGTACTGGGGTACCTGTGGGTGGGATCAGCGAGGGTACCTGAGCG	180
.81	TCAAGAGCATACCCTAGTGAGCGGGCTCCTCTGGGGGAGACCAGCGCGCTCCGGGCGCCT	240
1	GCCGGTTTGGGGGTGTCTCCTCCCGGGGCGCTATGGCGGCGCTGGCCAGTAGCCTGATCC  M A A L A S S L I R	300 10
301 11	GGCAGAAGCGGGAGGTCCGCGAGCCCGGGGGGAGCCGGCGGCGCGCGC	360 30
361 31	TGTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCCTGCTGTCCAAGG	420 50
121 51	TGCGACTGTGCGGGGGGGGCCGGGCCGGGCCGGGGCCCGGAGCCTCAAAG R L C G G R P A R P D R G P E P Q L K G	480 70
481 71	GCATCGTCACCAAACTGTTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCGACGGAA I V T K L F C R Q G F Y L Q A N P D G S	540 90
541 91	GCATCCAGGGCACCCCAGAGGATACCAGCTCCTTCACCCACTTCAACCTGATCCCTGTGG I Q G T P E D T S S F T H F N L I P V G	600 110
601	GCCTCCGTGTGGTCACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGCTG	660
111	LRVVTIQSAKLGHYMAMNAE	130
661 131	AGGGACTGCTCTACAGTTCGCCGCATTTCACAGCTGAGTGTCGCTTTAAGGAGTGTGTCT G L L Y S S P H F T A E C R F K E C V F	720 150
721 151	TTGAGAATTACTACGTCTGTACGCCTCTCTACCGCCAGCGTCGTTCTGGCCGGG ENYYVLYASALYRQRRSGRA	780 170
781 171	CCTGGTACCTCGGCCTGGACAAGGAGGGCCAGGTCATGAAGGGAAACCGAGTTAAGAAGA W Y L G L D K E G Q V M K G N R V K K T	840 190
841 191	CCAAGGCAGCTGCCCACTTTCTGCCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTT K A A A H F L P K L L E V A M Y Q E P S	900 210
901 211	CTCTCCACAGTGTCCCGAGGCCTCCCCTTCCAGTCCCCCTGCCCCCTGAAATGTAGTCC L H S V P E A S P S S P P A P *	960 226
961	CTGGACTGGAGGTTCCCTGCACTCCCAGTGAGCCAGCCACCACCACAACCTGTCTCCCAG	102

## Figure 1B

1021	TCCTGCTCTCACCCCTGCTGCCACACACACCCCTGAGCAGCCAGGTCCCACTAGGTGCT	1080
1081	CTACCCTGAGGGAGCCTAGGGGCTGACTGTGACTTCCGAGGGTGCTGAGCACCCTTAGAT	1140
1141	CTTTGGGCCTAGGAGGGGATCTCTGAAGATGGTCCTGGCTGATCACT	1200
1201	TCTTTCTTTCCACACTCACACACCCCATGTCCTTTTCCTGAGATGGCGCTGGGAGTTCC	1260
1261	CACATGGACAGCCAGGGCATAAACACTTCCCACCCCGGATCAGACAGTTCCCTGGAG 131	7

Figure 2

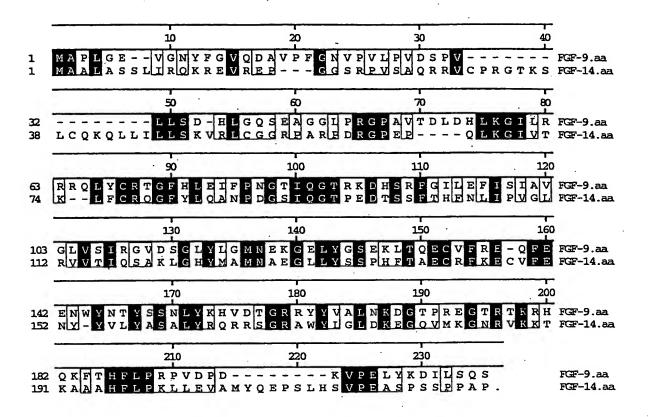


Figure 3

